

ABSTRACT

The present invention provides protein fragment complementation assays for drug discovery, in particular to identify compounds that activate or inhibit cellular pathways. Based on the selection of an interacting protein pair combined with an appropriate PCA reporter, the assays may be run in high-throughput or high-content mode and may be used in automated screening of libraries of compounds. The interacting pair may be selected by cDNA library screening; by gene-by-gene interaction mapping; or by prior knowledge of a pathway.

Fluorescent and luminescent assays can be constructed using the methods provided herein. The selection of suitable PCA reporters for high-throughput or high-content (high-context) assay formats is described for a diversity of reporters, with particular detail provided for examples of monomeric enzymes and fluorescent proteins. Methods are described for constructing such assays for one or more steps in a biochemical pathway; testing the effects of compounds from combinatorial, natural product, peptide, antibody, nucleic acid or other diverse libraries on the protein or pathway(s) of interest; and using the results of the screening to identify specific compounds that activate or inhibit the protein or pathway(s) of interest. Single-color and multi-color assays are disclosed. Further disclosed are universal expression vectors with cassettes that allow the rapid construction of assays for a large and diverse number of gene/reporter combinations. The development of such assays is shown to be straightforward, providing for a broad, flexible and biologically relevant platform for drug discovery.